

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

December 15, 2003, 14:57:24 ; Search time 20 Seconds

1490.615 Million cell updates/sec

(without alignments)

Title:	US-09-831-805A-6	30	7	2.3	297	2	AB3037	hypothetical prote	
Perfect score:	310	31	7	2.3	297	2	A81002	conserved hypothetical	
Sequence:	1 MALRRPPRLRLCARLPPFFL.....VNYIRTDEEGDFRKSSSFVI 310	32	7	2.3	299	2	A98249	nirrate transport	
Scoring table:	OLIGO	33	7	2.3	300	2	A82017	probable lipoprote	
	Gapop 60.0 , Gapext: 60.0	34	7	2.3	302	2	B70471	heat shock protein	
Searched:	283308 seqs, 9616802 residues	35	7	2.3	306	2	149139	lymphotoxin-beta -	
Word size :	0	36	7	2.3	314	2	AG3093	hypothetical prote	
Total number of hits satisfying chosen parameters:	283308	37	7	2.3	314	2	C98193	sugar transport system	
Minimum DB seq length: 0		38	7	2.3	314	2	T27302	hypothetical prote	
Maximum DB seq length: 200000000		39	7	2.3	333	2	I38974	G-protein-coupled	
Post-processing: Listing first 100 summaries		40	7	2.3	343	2	H95879	probable sugar ABC	
Database :	PIR 76:*	41	7	2.3	346	2	D75303	conserved hypothetical	
	1: pir1:*	42	7	2.3	362	2	G75614	GGDP family prote	
	2: pir2:*	43	7	2.3	375	2	T46378	hypothetical prote	
	3: pir3:*	44	7	2.3	376	2	F71815	hypothetical prote	
	4: pir4:*	45	7	2.3	380	2	E88421	probable R74.2 [imp	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		46	7	2.3	382	2	T24963	hypothetical prote	
SUMMARIES		47	7	2.3	391	2	E72539	probable sugar ABC	
Result No.	Score	Query Match Length	DB ID	Description	48	7	2.3	392	1 RWHUPD
					49	7	2.3	392	2 B44194
					50	7	2.3	400	2 T24258
					51	7	2.3	402	2 T04348
					52	7	2.3	402	2 G83367
					53	7	2.3	403	1 GRECY
					54	7	2.3	403	2 G90955
					55	7	2.3	403	2 D85804
					56	7	2.3	417	1 RWHUPA
					57	7	2.3	417	2 A44194
					58	7	2.3	420	2 T36532
					59	7	2.3	421	2 D82127
					60	7	2.3	431	2 D81282
					61	7	2.3	437	2 AE1849
					62	7	2.3	454	2 S31278
					63	7	2.3	463	2 D84055
					64	7	2.3	481	2 S69808
					65	7	2.3	490	2 A96556
					66	7	2.3	491	1 O4RBPC
					67	7	2.3	491	2 S31277
					68	7	2.3	491	2 P450
					69	7	2.3	491	2 S35665
					70	7	2.3	503	2 E83490
					71	7	2.3	503	2 E87628
					72	7	2.3	523	2 B95922
					73	7	2.3	524	2 A31318
					74	7	2.3	524	2 C95268
					75	7	2.3	558	2 B87098
					76	7	2.3	558	2 G70879
					77	7	2.3	595	2 H69345
					78	7	2.3	618	2 A36907
					79	7	2.3	629	2 AD1130
					80	7	2.3	643	2 A41130
					81	7	2.3	671	2 PH0268
					82	7	2.3	688	2 H83070
					83	7	2.3	689	2 D83501
					84	7	2.3	690	2 C36907
					85	7	2.3	693	1 S38427
					86	7	2.3	698	1 A47203
					87	7	2.3	705	2 T16088
					88	7	2.3	709	2 C87258
					89	7	2.3	716	2 AB1700
					90	7	2.3	721	2 S56580
					91	7	2.3	721	2 A98293
					92	7	2.3	721	2 D86934
					93	7	2.3	741	2 H90607
					94	7	2.3	747	2 T40728
					95	7	2.3	758	1 S45477
					96	7	2.3	780	2 T29580
					97	7	2.3	788	2 T4262
					98	7	2.3	789	2 E84236
					99	7	2.3	798	2 T48304
					100	7	2.3	815	2 H96494

ALIGNMENTS

RESULT 1

MHC class I lymphocyte antigen - human (fragment)

C;Species: Homo sapiens (man)

C;Accession: 168750 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000

R;Pohla, H.; Kwon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.

Immunogenetics 28, 291-307, 1989

A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B a

A;Reference number: 154457; MUID:89233295; PMID:2714852

A;Accession: 168750

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-290 <REG>

C;Cross-references: GB:MB28207; NID:9576478; PIDN:AAA53259.1; PIDN:9576479

F;144-209/domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 290;

Best Local Similarity 100.0%; Pred. No. 5; 9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256

Db 241 VLVVLAVL 248

RESULT 2

probable RING zinc finger protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: A86406

R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anseen, N.F.; Hughes, B.; Ruizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, G.; Yu, D.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86411; MUID:21016719; PMID:1130712

A;Accession: A86406

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-336 <STO>

C;Cross-references: GB:AE005172; NID:911024872; PIDN:AAG26956.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1.

RESULT 3

HLHUC4

MHC class I histocompatibility antigen HLA-C4 alpha chain - human

C;Species: Homo Sapiens (man)

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999

C;Accession: A24512

R;Davidson, W.F.; Krebs, M.; Khouri, G.; Jay, G.

A;Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonucleotides.

A;Cross-references: GB:ML1886; NID:9184173; PIDN:AAA52665.1; PID:9386777

A;Reference number: A92500; MUID:86033791; PMID:3863816

A;Accession: A24512

A;Map Position: 6p21.3-6p21.3

A;Molecule type: DNA

A;Cross-references: GB:ML1886; NID:9184173; PIDN:AAA52665.1; PID:9386777

C;Genetics:

A;Gene: GDB:HLA-C

A;Cross-references: GDB:119311; OMIM:142840

A;Residue: 1-342 <DNV>

C;Superfamily: class I histocompatibility antigen; immunoglobulin homology <IMM>

C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.6%; Score 8; DB 1; Length 342;

Best Local Similarity 100.0%; Pred. No. 6-8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256

Db 293 VLVVLAVL 300

RESULT 4

BB2933

Type I restriction enzyme M protein, truncated homolog UU098 [imported] - Ureaplasma urealyticum

C;Species: Ureaplasma urealyticum

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Oct-2002

C;Accession: EB2933

R;Glaab, J.J.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor

A;Reference number: A82870

A;Accession: EB2933

A;Status: Preliminary

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: hsdM-1; UU098

A;Molecule type: DNA

A;Residues: 1-148 <GA>

A;Cross-references: GB:AB002110; GB:AF222894; NID:96899051; PIDN:AAF30504.1; GSPDB:GN001

C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 2.6%; Score 8; DB 2; Length 348;

Best Local Similarity 100.0%; Pred. No. 7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 RKEIDEV 130

Db 336 RKEIDEV 343

RESULT 5

JH0546

class I histocompatibility antigen Gogo-C0202 heavy chain precursor - lowland gorilla

C;Species: Gorilla gorilla gorilla (lowland gorilla)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

C;Accession: JH0546

R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.

J. Exp. Med. 174, 1491-1509, 1991

A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human a

A;Reference number: JH0534; MUID:92078860; PMID:1744581

A;Accession: JH0546

A;Molecule type: DNA

A;Residues: 1-366 <LW>

A;Cross-references: EMBL:X60249; NID:922882; PIDN:CAA42801.1; PID:922883

A;Experimental source: EBV-transformed B cell

C;Genetics:

A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1

C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

C;Keywords: transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

P;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0202 #status pre
 F;23-114/Domain: alpha-1 <ALL>
 F;115-206/Domain: alpha-2 <ALL>
 F;207-298/Domain: alpha-3 <AL3>
 F;220-285/Domain: immunoglobulin homology <IMM>
 F;299-366/Domain: intracellular #status predicted <INT>
 Query Match 2.6%; Score 8; DB 2; Length 366;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 249 VLVVLAVL 256
 Db 317 VLVLVLAVAL 324

RESULT 6
 JH0547
 class I histocompatibility antigen Gogo-C0203 heavy chain precursor - lowland gorilla
 C;Species: Gorilla gorilla gorilla (lowland gorilla)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C;Accession: JH0547
 R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
 J;Exp. Med. 174, 1491-1509, 1991
 A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
 A;Reference number: JH0534; MUID:92078860; PMID:1744581
 A;Molecule type: DNA
 A;Residues: 1-366 <LAW>
 A;Experimental source: EBV-transformed B cell
 C;Genetics:
 A;Introns: 25/1; 115/1; 207/1; 299/1; 319/1; 350/1; 366/1
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C;Keywords: transmembrane protein
 F;1-366/Domain: signal sequence:#status predicted <SIG>
 F;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0203 #status pre
 F;25-114/Domain: alpha-1 <ALL>
 F;115-206/Domain: alpha-2 <AL2>
 F;207-298/Domain: alpha-3 <AL3>
 F;220-285/Domain: immunoglobulin homology <IMM>
 F;299-366/Domain: intracellular #status predicted <INT>
 Query Match 2.6%; Score 8; DB 2; Length 366;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 249 VLVVLAVL 256
 Db 317 VLVLVLAVAL 324

RESULT 8
 JH0547
 HLA-C alpha chain - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
 C;Accession: JH0547
 R; Vilches, C.; Bunce, M.; de Pablo, R.; Herrero, M.J.; Krasl, M.
 Tissue Antigens 46, 19-23, 1995
 A;Reference number: 137078; MUID:96086482; PMID:7482492
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-366 <RES>
 A;Cross-references: EMBL:X83394; NID:9669131; PIDN:CAA42800.1; PID:922885
 C;Genetics:
 A;Gene: CW*0704
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
 F;220-285/Domain: immunoglobulin homology <IMM>
 Query Match 2.6%; Score 8; DB 2; Length 366;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 249 VLVVLAVL 256
 Db 317 VLVLVLAVAL 324

RESULT 7
 JH0545
 class I histocompatibility antigen Gogo-C0201 heavy chain precursor - lowland gorilla
 C;Species: Gorilla gorilla gorilla (lowland gorilla)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C;Accession: JH0545
 R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
 J;Exp. Med. 174, 1491-1509, 1991
 A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
 A;Reference number: JH0534; MUID:92078860; PMID:1744581
 A;Molecule type: DNA
 A;Residues: 1-366 <LAW>
 A;Experimental source: EBV-transformed B cell
 C;Genetics:
 A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
 C;Keywords: transmembrane protein
 F;1-366/Domain: signal sequence #status predicted <SIG>
 F;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0201 #status pre

P;25-114/Domain: alpha-1 <ALL>
 F;115-206/Domain: alpha-2 <ALL>
 F;207-298/Domain: alpha-3 <AL3>
 F;220-285/Domain: immunoglobulin homology <IMM>
 F;299-366/Domain: intracellular #status predicted <INT>
 Query Match 2.6%; Score 8; DB 2; Length 492;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 242 IGGIGGV 249
 Db 244 IGGIGGV 251

RESULT 9
 AB1013
 Probable membrane protein STM4415 [imported] - Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 03-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB1013
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Cameron, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB1013
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-492 <PDR>
 A;Cross-references: GB:AL513382; PIDN:CADD09203.1; PID:916505207; GSPDB:GN00176
 C;Genetics:
 A;Gene: STM4415
 Query Match 2.6%; Score 8; DB 2; Length 492;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 37 RPPRL 43

RESULT 15
T25730
hypothetical protein At2g19340 [imported] - *Arabidopsis thaliana*
N;Alternate names: hypothetical protein F27F23.14
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01282; E84575
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A;Description: *Arabidopsis thaliana* chromosome II BAC F27F23 genomic sequence.
A;Reference number: Z14177
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-173 <STO>
A;Cross-references: EMBLAC003058; NID:g313250; PID:g3135250
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.D.; Rounsley, S.D.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Kao, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayan, L.; Tallon, L.;
euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <STO>
A;Cross-references: GB:AE002093; NID:g3135264; PIDN:AA016464.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g19340; F27F23.14
A;Map position: 2

Query Match 2.3%; Score 7; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 RPPRL 11
Db 38 RPPRL 44

RESULT 16
B90241
hypothetical protein SS0903 [imported] - *Sulfolobus solfataricus*
C;Species: *Sulfolobus solfataricus*
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: B90241
R;She, Q.; Sing, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awazy, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Koza, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, E.
arrest, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: *Sulfolobus solfataricus* complete genome.
A;Reference number: A99139
A;Accession: B90241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <STO>
A;Cross-references: GB:AE005174; NID:g12516269; PIDN:AA057129.1; GSPDB:GN00145; UNGP:Z32
A;Experimental source: strain O157:H7, substrain ED933
C;Genetics:
A;Gene: 23235

Query Match 2.3%; Score 7; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 247 GGVVVL 253
Db 139 GGVVVL 145

RESULT 19
B90988
partial probable sensor kinase ECs2874 [similarity] - *Escherichia coli* (strain O157:H7,
C;Species: *Escherichia coli*
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C;Accession: B90988
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno-
A;Reference number: A99629; MUID:21156231; PMID:11238796
A;Accession: B90988
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-177 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAR36297.1; PID:913362343; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: Ecs2874

Query Match 2.3%; Score 7; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 GGYLVNL 253
Db 139 GGYLVNL 145

RESULT 20

T03627 GTP-binding protein Rab6 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C;Accession: T03627
A;Status: preliminary; translated from GB/EMBL/DDBJ
R;Harel, T.; Meekle, T.; Turck, F.; Nagy, F.
Plant Physiol. 108, 59-67, 1995

A;Title: Characterization of membrane-bound small GTP-binding proteins from Nicotiana ta
A;Reference number: Z14896; MUID:9503981; PMID:7704525
A;Accession: T03627
A;Molecule type: mRNA
A;Residues: 1-208 <HAT>
A;Cross-references: EMBL:129273; NID:9623585; PIDN:AAA7117.1; PID:9623586
A;Experimental source: strain SRL
C;Genetics:
A;Gene: Rab6
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F;10-125/Domain: translation elongation factor Tu homology <ETU>
F;12-125/Region: GTP-binding NGKD motif
F;15-225/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNLKSSN 38
Db 187 VNLKSSN 193

RESULT 21

T01588 GTP-binding protein At2g44610 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Mar-2001
C;Accession: T01588; F8480
R;Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, A.; Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.
A;Reference number: Z14284
A;Accession: T01588
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-208 <ROU>
A;Cross-references: EMBL:AC003672; NID:g3341671; PIDN: AAC27463.1; PID:93341681
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tailor, L.; euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: AB4420; MUID:2003487; PMID:1067197
A;Accession: F84880

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: GB:AE002093; NID:g3341681; PIDN: AAC27463.1; GSPDB:GN00139
C;Genetics:
A;Gene: F16B22.10; Att2g44610

A;Map position: 2
A;Introns: 39/3; 63/2; 93/1; 130/2; 160/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F;10-125/Domain: translation elongation factor Tu homology <ETU>
F;16-23/Region: nucleotide-binding motif A (P-loop)
F;122-125/Region: GTP-binding NKXD motif
F;152-154/Region: GTP-binding SAK/L motif

Query Match 2.3%; Score 7; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNLKSSN 38
Db 187 VNLKSSN 193

RESULT 22

F86888 Hypothetical protein yvia [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: E86888
R;Boletin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlund, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlund, A.; Reference number: E86625; MUID:21235186; PMID:11337471
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <SDQ>
A;Cross-references: GB:AE005176; PID:912725164; PIDN: AAK06207.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yvia

Query Match 2.3%; Score 7; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 GGIIGGY 249
Db 45 GGIIGGY 51

RESULT 23

T47268 Phosphatidylserine synthase [imported] - Helicobacter felis
C;Species: Helicobacter felis
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C;Accession: T47268
R;Bayle, D.; Wangler, S.; Weizsaecker, T.; Steinilber, W.; Volz, J.; Przybylski, M.; S. J. Bacteriol. 180, 317-329, 1998
A;Title: Properties of the P-type ATPases encoded by the copA operons of Helicobacter p
A;Reference number: Z22437; MUID:9810471; PMID:9440521
A;Accession: T47268
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-214 <HAY>
A;Cross-references: EMBL:AU001932; NID:g266038; PIDN: CAA05103.1; PID:92660541
A;Experimental source: strain ATCC 49179
C;Superfamily: Bacillus subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase; Bac
F;9-160/Domain: Bacillus subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase hor

Query Match 2.3%; Score 7; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 18 FPLLLP 24
 Db 172 FPLLLP 178

RESULT 24

T30456 occlusion-derived virus envelope protein odv-e25 - Lymantria dispar nuclear polyhedrosis virus LdMPV
 C;Species: Lymantria dispar nuclear polyhedrosis virus LdMPV
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
 C;Accession: T30456
 R;Kuino, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr, Virology 253, 17-34, 1999
 A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria dispar
 A;Reference number: 220836; MUID:99124785; PMID:9887315
 A;Accession: T30446
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-217 <RNU>
 A;Cross-references: EMBL:AFO81010; NID:93822334; PIDN:MAC70282.1; PID:g3822331
 C;Keywords: envelope protein

Query Match 2.3%; Score 7; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 54; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LVVLAVL 256
 Db 9 LVVLAVL 15

RESULT 25

G84315 cobalt transport protein [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: G84315
 R;NG, W.V.; Kennedy, S.P.; Malairas, G.G.; Borquiat, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leuthäuser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, H.; Alam, M.; Freitas, T.; Jung, J.H.; Alm, A.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504403; PMID:11016950
 A;Accession: G84315
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-255 <OLI>
 A;Cross-references: EMBL:AL009204; PIDN:CA15804.1; GSPDB:GN00070; SCOEDB:SC9B10.14
 A;Experimental source: strain A(3)(2)
 C;Genetics:
 A;Gene: SCOEDB:SC9B10.14
 C;Superfamily: transcription regulator GntR

Query Match 2.3%; Score 7; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 56; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 IELTVQV 137
 Db 233 IELTVQV 239

RESULT 26

PH0269 epidermal autoantigen 450K (clone PE450-B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 25-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 31-Oct-1997
 C;Accession: PH0269
 R;Fujiwara, S.; Kohno, K.; Iwamatou, A.; Naito, I.; Shinkai, H.
 A;Submitted to JIPID, July 1995
 A;Description: The 450kD epidermal autoantigen is a novel protein in plectin family.
 A;Reference number: PH0268
 A;Accession: PH0269
 A;Molecule type: mRNA
 A;Residues: 1-280 <FU>
 C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S

Query Match 2.3%; Score 7; DB 2; Length 280;
 Best Local Similarity 100.0%; Pred. No. 61; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 266 AVRRGYP 272
 Db 204 AVRRGYP 210

RESULT 26

A46056 Lymphotoxin beta - human
 C;Species: Homo sapiens (man)
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C;Accession: A46056
 R;Browning, J.L.; Ngam-ek, A.; Lawton, P.; DeMarinis, J.; Tizard, R.; Chow, E.P.; Hesic, Cell 72, 847-856, 1993
 A;Title: Lymphotoxin beta, a novel member of the TNF family that forms a heteromeric com
 A;Reference number: A46056; MUID:93208881; PMID:7916655

RESULT 26

H84023 phosphate ABC transporter (permease) BH2992 [imported] - Bacillus halodurans (strain C-1)
 C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: HB4123
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: HB4123
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-294 <SRO>
 A;Cross-references: GB:AP001517; GB:BA000004; NID:gi01175500; PIDN:BAB06711.1; GSPDB:GN00
 A;Experimental source: strain C-125
 A;Gene: BH992
 C;Superfamily: phoW protein

Query Match Score 7; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30

AB3037 hypothetical protein *nrtB* [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C;Species: *Agrobacterium tumefaciens* (strain C58, Dupont)
 C;Date: 11-Jan-2002 #sequence_change 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AB3037
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, D.; Guenther, D.; Kuryavina, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Teo, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, R.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A;Reference number: AB2577; MUID:2108550; PMID:11743193
 A;Accession: AB0317
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-297 <KUR>
 A;Cross-references: GB:AE008689; PIDN:AAL44712.1; PID:gi17742343; GSPDB:GN00187
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: nrtB
 A;Map position: linear chromosome
 C;Superfamily: Synechococcus nitrate transport protein nrtB

Query Match Score 7; DB 2; Length 297;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LVVLAVL 256
 Db 35 LVVLAVL 41

RESULT 31

A81022 conserved hypothetical protein *NMB2139* [imported] - *Neisseria meningitidis* (strain MC58)
 C;Species: *Neisseria meningitidis*
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C;Accession: A81002
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiognani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Veitia, A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:2015755; PMID:1070307
 A;Accession: A81002

RESULT 32

A98249 nitrate transport permease protein *nrtB* AGR_L_1888 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C;Species: *Agrobacterium tumefaciens* (strain C58, Dupont)
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C;Accession: A98249
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: A98249
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-299 <KUR>
 A;Cross-references: GB:AE007870; PIDN:AAK89515.1; PID:gi15159391; GSPDB:GN00170
 C;Genetics:
 A;Gene: AGR_L_1888
 A;Map position: linear chromosome
 C;Superfamily: Synechococcus nitrate transport protein nrtB

Query Match Score 7; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LVVLAVL 256
 Db 35 LVVLAVL 58

RESULT 33

A822017 probable lipoprotein NMA0225 [imported] - *Neisseria meningitidis* (strain 22491)
 C;Species: *Neisseria meningitidis*
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C;Accession: A822017
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jäger, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, M.; Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A;Reference number: A81775; MUID:2022556; PMID:10761919
 A;Accession: A822017
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-300 <PAR>
 A;Cross-references: GB:AL162752; GB:AL157959; NID:gi7378778; PIDN:CAB83536.1; PID:gi737899
 C;Experimental source: serogroup A, strain 22491
 C;Genetics:
 A;Gene: NMA0225

Query Match Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 ABILGKT 98
 Db 100 ABILGKT 106

Db 103 AEILGKT 109
 RESULT 34
 B70471 heat shock protein X - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Aug-1999
 C;Accession: B70471
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; On
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:9819666; PMID:9537320
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-302 <RQF>
 A;Cross-references: GB:AB000766; NID:92984215; PIDN:AA007747.1; PID:92984218; GB:AB00065
 A;Experimental source: strain VF5
 C;Genes:
 A;Superfamily: heat-shock protein htpX
 Query Match 2.3%; Score 7; DB 2; Length 302;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 242 IGGIGG 248
 Db 31 IGGIGG 37
 RESULT 35
 I49139 Lymphotoxin-beta - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I49139; I49138; I49076
 R;Lawton, P.; Nelson, J.; Tizard, R.; Browning, J.L.
 J; Immunol. 134, 239-246, 1995
 A;Title: Characterization of the mouse lymphotoxin-beta gene.
 A;Reference number: I49138; MUID:93088371; PMID:7995944
 A;Accession: I49139
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-306 <REB>
 A;Cross-references: EMBL:U16985; NID:9577830; PIDN:AAA70089.1; PID:9577831
 A;Accession: I49138
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-306 <REB>
 A;Cross-references: EMBL:U16984; NID:9577431; PIDN:AA860493.1; PID:9577432
 A;Cross-references: EMBL:U16984; NID:9577431; PIDN:AA860493.1; PID:9577432
 R;Potholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov, S.V.; Novob
 proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995
 A;Title: Cloning and expression analysis of the murine lymphotoxin beta gene.
 A;Reference number: A55602; MUID:95148600; PMID:7846035
 A;Accession: I49076
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-306 <RB2>
 A;Cross-references: EMBL:U12029; NID:9515508; PIDN:AA67716.1; PID:9515509
 C;Genes:
 A;Gene: LT-beta
 A;Introns: 54/3; 160/1
 Query Match 2.3%; Score 7; DB 2; Length 306;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 252 LVLAVAL 258
 Db 40 LVLAVAL 46
 RESULT 36
 AG3093 hypothetical protein Atu4371 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AG3093
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monk, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 Bter, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AG3093
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-314 <KUR>
 A;Cross-references: GB:AE008689; PIDN:ALA5165.1; PID:917742841; GSPDB:GN00187
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Genetics: Atu4371
 A;Map position: linear chromosome
 C;Superfamily: 1-arabinose transport system permease arah
 Query Match 2.3%; Score 7; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 250 LVVLAVL 256
 Db 16 LVVLAVL 22
 RESULT 37
 CG8193 sugar transport system permease protein homolog (AF036920) [imported] - Agrobacterium tum
 C;Species: Agrobacterium tumefaciens
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C;Accession: C98193
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourolo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; MUID:21608551; PMID:11743194
 A;Accession: C98193
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-314 <KUR>
 A;Cross-references: GB:AE007870; PIDN:AAK89069.1; PID:915158867; GSPDB:GN00170
 C;Genetics:
 A;Genes: AGR_L_991
 A;Map position: linear chromosome
 C;Superfamily: 1-arabinose transport system permease arah
 Query Match 2.3%; Score 7; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 250 LVVLAVL 256
 Db 16 LVVLAVL 22
 RESULT 38
 T27302 hypothetical protein Y68A4A.6 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T27302
 R;Steward, C.

submitted to the EMBL Data Library, January 1998
 A;Reference number: 220340
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-324 <WIL>
 A;Cross-references: EMBL:AL021503; PIDN:CAA16423.1; GSPDB:GN00023; CESP:Y68A4A.6
 A;Experimental source: clone Y68A4A
 C;Genetics:
 A;Gene: CESP:Y68A4A.6
 A;Map position: 5
 A;Introns: 48/3; 88/2; 187/3; 242/3
 Query Match 2.3%; Score 7; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 19 FFLFLFR 25
 Db 235 FFLFLFR 241

RESULT 39
 G protein-coupled receptor 8 - human
 C;Species: Homo sapiens (man)
 C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
 C;Accession: I38974
 R;O'Dowd, B. F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
 Genomics 28, 84-91, 1995
 A;Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
 A;Reference number: A57647; MUID:96070436; PMID:7590751
 A;Accession: I38974
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-333 <RBS>
 A;Cross-references: EMBL:U22492; NID:9553234; PIDN:AAC50198.1; PID:9553235
 C;Genetics:
 A;Gene: GDB:GPR8
 A;Cross-references: GDB:371716; OMIM:600730
 A;Map position: 20q13.3-20q13.3
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 2.3%; Score 7; DB 2; Length 333;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 249 VLVVLAV 255
 Db 262 VLVVLAV 268

RESULT 40
 H95879
 probable sugar ABC transporter permease protein SMB0318 [imported] - Sinorhizobium meliloti
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C;Accession: H95879
 R;Finan, T.M.; Weidner, S.; Wong, K.J.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1,683-kb pSYM_B megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: H95879
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-343 <KIR>
 A;Cross-references: GB:AL591985; PIDN:CA48704.1; PID:915140177; GSPDB:GN00167
 A;Experimental source: strain 1021, megaplasmid pSYM
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 L.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001

RESULT 41
 D75303
 conserved hypothetical protein - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: D75303
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S., M.; Shem, M.; Vaishnaveen, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,
 S.; Smith, H.O.; Ventter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: D75303
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-46 <WHI>
 A;Cross-references: GB:AE002053; GB:AE000513; NID:96459999; PIDN:AAF11754.1; PID:9646000
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR2205
 A;Map position: 1

Query Match 2.3%; Score 7; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 248 GVLVVLVA 254
 Db 333 GVLVVLVA 339

RESULT 42
 G75614
 GGDEF family protein - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: G75614
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S., M.; Shem, M.; Vaishnaveen, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,
 S.; Smith, H.O.; Ventter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: G75614
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-362 <WHI>
 A;Cross-references: GB:AB001862; GB:AE001825; NID:96450468; PIDN:AAF12191.1; PID:9646048
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR20181
 A;Map Position: 2

Query Match 2.3%; Score 7; DB 2; Length 362;

		Best Local Similarity 7; Conservative 0; Pred. No. 76; Mismatches 0; Indels 0; Gaps 0;
Matches 7;	Conservative 0;	Mismatches 0;
Qy 257 ALITLG1 263		A;Title: Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology, Science 282, 2012-2018, 1998
C;Species: Homo sapiens (man)		A;Reference number: A75000; MUID:9906913; PMID:9851916
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000		A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
C;Accession: T46378		A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
Db 178 ALITLG1 184		A;Accession: R8421
RESULT 43		A;Status: preliminary
T46378 hypothetical protein DKFP434G0719.1 - human (fragment)		A;Molecule type: DNA
Qy C;Species: Homo sapiens (man)		A;Residues: 1-380 <STO>
C;Accession: T46378		A;Cross-references: EMBL:AL137725
Db A;Experimental source: adult testis; clone DKFP434G0719		A;Reference number: 223031
C;Genetics:		A;Note: RT4
A;Note: DKFP434G0719.1		A;Map position: 3
Query Match 2.3%; Score 7; DB 2; Length 375;		Query Match 2.3%; Score 7; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 79; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Best Local Similarity 100.0%; Pred. No. 80; Mismatches 0; Indels 0; Gaps 0;
Qy 266 AYRRGYF 272		Qy 266 AYRRGYF 272
Db 317 AYRRGYF 323		Db 115 AYRRGYF 121
RESULT 44		RESULT 46
F71815 hypothetical protein Jhp1379 - Helicobacter pylori (strain J99)		T24963 hypothetical protein T1B03.3 - Caenorhabditis elegans
A;Species: Helicobacter pylori		C;Species: Caenorhabditis elegans
A;Variety: strain J99		C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C;Accession: F71815		C;Accession: T24963
R;Alt, R.A., Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Marberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen		R;McCurdy, A.
A;Reference: PT1815		submitted to the EMBL Data Library, November 1995
A;Cross-references: GB:AE001560; GB:AE001439; NID:g4155981; PIDN:AAD06950.1; PID:g415598		A;Accession: Z19962
A;Experimental source: strain J99		A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Genetics:		A;Molecule type: DNA
A;Residue: 1-76 <ARN>		A;Residues: 1-382 <WIL>
A;Cross-references: GB:AE001560; GB:AE001439; NID:g4155981; PIDN:AAD06950.1; PID:g415598		A;Cross-references: EMBL:Z68119; PIDN:CAA92193.1; GSPPDB:GN00028; CESP:T18D3.3
A;Experimental source: clone T18D3		A;Experimental source: clone T18D3
A;Genetics:		C;Genetics:
C;Accession: CESP:T18D3.3		A;Gene: CESP:T18D3.3
A;Map position: X		A;Map position: X
A;Introns: 34/2; 72/1; 142/1; 193/2; 254/3; 290/1; 325/3		A;Introns: 34/2; 72/1; 142/1; 193/2; 254/3; 290/1; 325/3
Query Match 2.3%; Score 7; DB 2; Length 382;		Query Match 2.3%; Score 7; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 80; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Best Local Similarity 100.0%; Pred. No. 80; Mismatches 0; Indels 0; Gaps 0;
Qy 248 GVLVWLA 254		Qy 248 GVLVWLA 254
Db 158 GVLVWLA 164		Db 158 GVLVWLA 164
RESULT 45		RESULT 47
C;Superfamily: conserved hypothetical integral membrane protein RP1486		E72539 hypothetical protein APE1602 - Aeropyrum pernix (strain K1)
Query Match 2.3%; Score 7; DB 2; Length 376;		C;Species: Aeropyrum pernix
Best Local Similarity 100.0%; Pred. No. 79; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
Qy 9 LRLCRL 15		C;Accession: E72539
Db 220 LRLCRL 226		R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kita, DNA Res. 6, 83-101, 1999
C;Accession: E8421		A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
R;Anonymous, The C. elegans Sequencing Consortium.		A;Reference number: A72450; MUID:9931039; PMID:10382966
RESULT 45		A;Accession: E72539
E88421 protein R74.2 [imported] - Caenorhabditis elegans		A;Status: preliminary
C;Species: Caenorhabditis elegans		A;Molecule type: DNA
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001		A;Residues: 1-391 <RAW>
C;Accession: E88421		A;Cross-references: DDBJ:AP000062; NID:g510524; PIDN:BA00602.1; PID:d1044388; PID:g510
R;Anonymous, The C. elegans Sequencing Consortium.		A;Experimental source: Strain K1
		C;Genetics:
		C;Accession: APB1602

Query Match 2.3%; Score 7; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy |||||||

Db 64 RPPRLRL 11

Qy |||||||

Db 64 RPPRLRL 70

Qy |||||||

Db 132 BLTVQVK 138

Qy |||||||

Db 324 BLTVQVK 330

N;Alternate names: poliovirus receptor precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997

C;Accession: A3104; B3195

R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Izuka, N.; Takeuchi, K.; Take

EMBO J. 9; 3217-3224; 1990

A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted

A;Reference number: S12048; MUID:91006015; PMID:2170108

A;Accession: A31024

A;Molecule type: DNA

A;Residues: 1-352 <R01>

A;Cross-references: EMBL:X64116

A;Note: 67-Ala was also found

Cell; Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.

Cell 56; 855-865; 1989

A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e

A;Reference number: A90910; MUID:89168426; PMID:2538245

A;Accession: B1496

A;Molecule type: mRNA

A;Residues: 1-66; A, 68-392 <MEN>

C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f

C;Genetics:

A;Gene: GDP; PVR; PV5

A;Cross-references: GDB:120324; OMIM:173850

A;Map position: 19q13.2

A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1

C;Superfamily: poliovirus receptor; immunoglobulin homology

C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-392/Product: poliovirus receptor delta #status predicted <EXT>

F;21-343/Domain: extracellular #status predicted <EXT>

F;42-125/Domain: immunoglobulin homology <IMM1>

F;159-223/Domain: immunoglobulin homology <IMM2>

F;259-314/Domain: immunoglobulin homology <IMM3>

F;344-367/Domain: transmembrane #status predicted <TMN>

F;368-392/Domain: intracellular #status predicted <INT>

F;49-123,-66-221,266-312/disulfide bonds: #status predicted

F;105,120,188,-218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 2.3%; Score 7; DB 1; Length 392;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 BLTVQVK 138

Db 324 BLTVQVK 330

A;Molecule type: DNA
 A;Residues: 1-392 <R01>
 A;Cross-references: GB:94817
 C;Superfamily: poliovirus receptor; immunoglobulin homology <IM>
 F;259-314/Domain: immunoglobulin homology <IM>

Query Match 2.3%; Score 7; DB 2; Length 392;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 7; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy |||||||

Db

Qy |||||||